Salmonella fecal shedding in pigs from birth to market and its association with the presence of *Salmonella* in palatine tonsils and submandibular lymph nodes at slaughter

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Abstract

Salmonella is an important cause of foodborne illnesses in humans. Food-producing animals, including swine, are a major source of *Salmonella* in food products. This study investigated on farm *Salmonella* fecal shedding in pigs at different production stages — from weaning to marketing — and its association with the presence of *Salmonella* in tissues at slaughter. Fourteen groups from 8 commercial farrowing sources (N = 809 pigs) were monitored 5 times from birth to slaughter. Fecal and tissue samples were collected from pigs and cultured for *Salmonella*. A survey was conducted to collect farm management information. A multi-level mixed-effects logistic regression modelling method was used to analyze *Salmonella* shedding over time and the association between *Salmonella* shedding and the presence of *Salmonella* in tissue samples. *Salmonella* was recovered from 13% (421/3339) of fecal samples collected from 809 pigs over the course of the study. Overall, 35% (284) of pigs shed *Salmonella* at least once, while 12% (99) shed more than once. *Salmonella* shedding increased as pigs aged ($P = 0.01$) and increased in the summer months ($P < 0.01$). *Salmonella* was isolated from tissue samples collected from 23% (134/580) of pigs; however, the presence of *Salmonella* at slaughter was not associated with on farm shedding. The seasonal trend in *Salmonella* shedding and its association with age may be used to identify high-risk groups and implement more effective control measures accordingly. The identification of repeat shedders warrants interventions that target this source of infection on swine farms.

Résumé

Salmonella *est une cause importante de maladies d'origine alimentaire chez les humains. Les animaux de rente, incluant le porc, sont une source majeure de* Salmonella *dans les produits alimentaires. Au cours de la présente étude nous avons examiné l'excrétion fécale de* Salmonella *à la ferme à différents stades de la production — du sevrage jusqu'à la mise en marché — et sont association avec la présence de* Salmonella *dans les tissus au moment de l'abattage. Quatorze groupes provenant de huit sources commerciales de mise-bas (*N = *809 porcs) ont été surveillés cinq fois entre la naissance et l'abattage. Des échantillons de fèces et de tissus ont été prélevés des porcs et cultivés pour* Salmonella. *Un sondage a été mené pour amasser des informations sur la gestion de la ferme. Une méthode de modélisation de régression logistique à effets mixtes de niveaux multiples a été utilisée pour analyser l'excrétion de* Salmonella *dans le temps et l'association entre l'excrétion de* Salmonella *et la présence de* Salmonella *dans les échantillons de tissus.* Salmonella *a été isolé de 13 % (421/3339) des échantillons de fèces prélevés des 809 porcs durant la durée de cette étude. Au total, 35 % (284) des porcs ont excrété* Salmonella *au moins une fois, alors que 12 % (99) ont excrété plus d'une fois. L'excrétion de* Salmonella *augmentait à mesure que les porcs vieillissaient (*P = *0,01) et augmentait durant les mois d'été (*P < *0,01).* Salmonella *a été isolé d'échantillons de tissu prélevés de 23 % (134/580) des porcs; toutefois, la présence de* Salmonella *au moment de l'abattage n'était pas associée avec l'excrétion à la ferme. La tendance saisonnière dans l'excrétion de* Salmonella *et son association avec l'âge pourraient être utilisées afin d'identifier les groupes à risque élevé et mettre en place selon le cas des méthodes de maitrise plus efficaces. L'identification d'excréteurs à répétition justifie des interventions qui ciblent cette source d'infection sur les fermes porcines.*

(Traduit par Docteur Serge Messier)

Introduction

Salmonella continues to be one of the most important causes of foodborne gastrointestinal illness in humans. In Canada, non-typhoidal salmonellosis is estimated to be the fourth leading cause of all foodborne illnesses (1). Food producing animals are the main cause of human salmonellosis, through the consumption of contaminated food of animal origin or produce that was either grown with livestock manure used as fertilizer or was accidentally contaminated (2,3). *Salmonella* is frequently found on swine farms (4,5) and one study in the United States reported that 9% of food-borne *Salmonella* outbreaks with a known cause were attributed to

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pork products (6). *Salmonella* is also responsible for economic losses in the swine industry from lost productivity; for example, clinical salmonellosis can lead to increased drug use, reduced weight gain and feed gain ratios, increased time to market, and loss of premiums due to variability in carcass weight (7,8).

The presence of intermittent shedders and the variable nature of *Salmonella* infection over time present limitations to point-prevalence studies (9). A clear understanding of the shedding patterns over the entire production stage on commercial pig farms is crucial for implementing effective monitoring and control measures.

Salmonella reduction at the farm level is important to mitigate *Salmonella* transmission from pigs to humans. Some pigs shed *Salmonella* in feces despite appearing healthy. These subclinical carriers can exacerbate levels of *Salmonella* in the barn and slaughterhouse and infect pigs with no previous exposure during transportation and lairage. In addition, there is potential for cross-contamination of carcasses during processing. Although some studies have shown that on farm *Salmonella* shedding may predict the presence of *Salmonella* at slaughter (10), others have found no association between *Salmonella* shedding and its presence at slaughter (11,12).

Salmonella is considered a hazard at the slaughterhouse. Various processes such as bleeding and evisceration have been identified as critical control points, during which the sterile muscle tissue may be exposed to contaminants from the digestive tract or the environment (13,14). The number of infected pigs arriving at the slaughterhouse is a risk factor for contamination during processing (15); therefore, it is necessary to decrease the presence of *Salmonella* on swine farms. The objectives of this study were to assess the *Salmonella* shedding patterns in pigs from birth to market age and to determine if there is a correlation between on farm *Salmonella* shedding and *Salmonella* colonization at slaughter.

Materials and methods

The University of Guelph Animal Care Committee approved all animal use in this study.

Study design

Fourteen groups of pigs were selected from a convenience sample of 8 farrowing sources located in southwestern Ontario, with 6 farrowing sources contributing 2 cohorts each. Piglets in Cohort 1 were born between May and August and piglets in Cohort 2 were born between October and January. For each group on each farm, 8 to 10 sows were selected; from the litters of each sow, 4 to 8 piglets were selected within 96 h of birth and individually identified with an ear tag. As part of a larger project, during the nursery stage, half of the selected piglets in each litter were fed a high complexity diet (standard in commercial nurseries) while the remaining ear-tagged pigs were fed a low complexity diet, replacing animal-based proteins with plant-based proteins. After the nursery period, all pigs consumed the feed routinely used by that particular farm. A survey with a mix of open- and close-ended questions was distributed to producers regarding operation size and type, feed type and supplier, genetic supplier, vaccination program and health records, pig flow and biosecurity practices, as well as in-feed antibiotic and therapeutic zinc use.

Pig movement

In total, 14 groups of pigs originated from 8 distinct farrowing sources. Only one group was housed in a farrow-to-finish operation, while the second group of pigs from this farm used an off-site finisher barn. The remaining 12 groups used an off-site nursery and off-site finisher barns. The farrowing and nursery sites remained consistent between Cohort 1 and Cohort 2 for all farms in the study; however, on 3 farms, animals in Cohort 2 were housed in a different finisher barn than in Cohort 1 in order to accommodate space requirements in the production system, for a total of 26 barns.

Sample collection

Pigs were monitored from birth until slaughter. Fecal samples were either collected into sterile bags as pigs defecated or by rectal swabs (Starplex collector vials; VWR, Mississauga, Ontario) at weaning and at the end of the nursery, grower, and finisher periods. In addition, rectal swabs were collected from piglets prior to 4 d of age in 7 groups (on 2 farms in Cohort 1 and 5 farms in Cohort 2). Over the course of the farm study, 146 pigs were lost; 23 died before the first sampling period and 55 (from one group) were shipped to a slaughterhouse without notifying the researchers. All fecal samples and rectal swabs were transported in an insulated container on ice to the laboratory.

A subset of pigs from each group was shipped (between 30 and 120 km) to a slaughterhouse where pigs were held overnight before processing. At slaughter, palatine tonsils and submandibular lymph node samples were cut from the carcass and placed in a sterile bag by members of the research team, with the exception of one farm, in which only tonsil samples were collected.

Salmonella isolation

For each fecal and tissue sample, 10 g of material was transferred into a stomacher bag (Seward Laboratory Systems, Bohemia, New York, USA) and homogenized in 50 mL of tetrathionate broth (TTB) (Oxoid, Nepean, Ontario) using a Seward Stomacher 400 Circulator (Seward Laboratory Systems). Swabs were cultured in 5 mL of TTB. All samples were incubated for 24 h at 37°C. Then, 0.1 mL of TTB culture was inoculated into 9.9 mL of Rappaport Vassiliadis (RV) broth (Oxoid) and incubated at 42°C for 24 h. Finally, a loopful of RV culture was streaked onto xylose-lysine-tergoitol 4 agar (Becton Dickinson, Baltimore, Maryland, USA) and incubated at 37°C for 24 to 72 h. Colonies consistent with *Salmonella* were then plated on Luria agar (Becton Dickinson, Grayson, Georgia, USA) and incubated for 24 h before confirmation with *Salmonella* O Antiserum Poly A-I & Vi (Becton Dickinson). One isolate per sample was stored at −80°C. All samples were cultured immediately except for fecal samples from 4 visits, which were frozen for 6 to 10 wk at −20°C, and tissue samples from 2 slaughter visits, which were frozen for 2 wk at −20°C before culturing.

Data analysis

Data were entered into an Excel spreadsheet (Microsoft, Redmond, Washington, USA) for cleaning and then imported to Stata (Stata/IC-14 StataCorp, College Station, Texas, USA) for analysis.

Table I. Number of fecal *Salmonella* shedding in pigs in Cohort 1 and Cohort 2.

Number of shedding	Number of pigs (%)	
	Cohort 1	Cohort 2
0	321 (68.3)	224 (62.4)
1	106 (22.6)	79 (22.0)
2	37 (7.9)	36 (10.0)
3	3 (0.6)	13 (3.6)
4	3 (0.6)[a]	5 (1.4)
5	—	2 (0.6)[b]

[a] Maximum shedding for Cohort 1 is 4 (n = 470).

[b] Maximum shedding for Cohort 2 is 5 (n = 359).

***Salmonella* shedding in feces across stages of production.** A multilevel mixed-effects logistic regression model with pig, sow, and farm as random effects was fitted to analyze *Salmonella* shedding in feces across the stages of production. The dependent variable was the presence of *Salmonella* in either feces or rectal swab.

***Salmonella* in tissue samples and its association with fecal shedding.** Multilevel mixed-effects logistic regression models with sow and farm as random effects were fitted to analyze the associations between the presence of *Salmonella* in tissue samples and fecal shedding. The dependent variable was defined as the presence of *Salmonella* in palatine tonsil or submandibular lymph node harvested from each pig at slaughter. *Salmonella* status on farm was defined by whether or not the pig shed *Salmonella* at least once over the course of the farm study (model 1), the number of times a pig shed *Salmonella* (range: 0 to 5; model 2), and *Salmonella* shedding at each stage of production (model 3). Additional models were also fitted to look at associations between fecal shedding on farm and presence of *Salmonella* in each tissue sample separately (tonsil and lymph node).

The independent variables included in the univariable analysis were age, herd size (number of sows, nursery, and finisher pigs), herd type (closed or open), farrowing schedule (weekly or batch), flow at each stage (all-in-all-out or continuous), presence of a shower (yes or no), Danish entrance (yes or no), in-feed zinc (nutritional if $<$ 250 ppm or therapeutic if $>$ 250 ppm), cohort (1 or 2), and the season in which a sample was collected [spring (March 21 to June 20), summer (June 21 to September 20), fall (September 21 to December 20), winter (December 21 to March 20)], as well as nursery diet (high complexity or low complexity). Only one farm was antibiotic-free. The data were analyzed excluding this farm, but no difference was seen compared to the model in which this farm was included. The number of times pigs were transported was recorded (range: 0 to 2) as well as shipping distance to the slaughterhouse (range: 25 to 129 km). Lairage time was consistent for each pig sampled at slaughter and was not analyzed. Bacteriological culture of trucks used for transportation could not be performed before or after shipping due to the number of groups of pigs and the number of times they were shipped.

Univariable analysis was performed using a single logistic regression method and variables with a $P < 0.2$ were considered for inclusion in the multivariable models. Collinearity between independent variables was tested; a Pearson correlation coefficient of 0.6 or higher indicated co-linear variables. A manual forward stepwise method was used to build the multivariable models. The statistical significance association of independent variables with the outcome was assessed by likelihood ratio test and variables with $P < 0.05$ were included in the final model. A partial F-test was used to test the significance of group variables. A variable was considered confounding if it altered the coefficient of the main effect by at least 15%. Interaction terms between variables were tested and included in the model if they were significant.

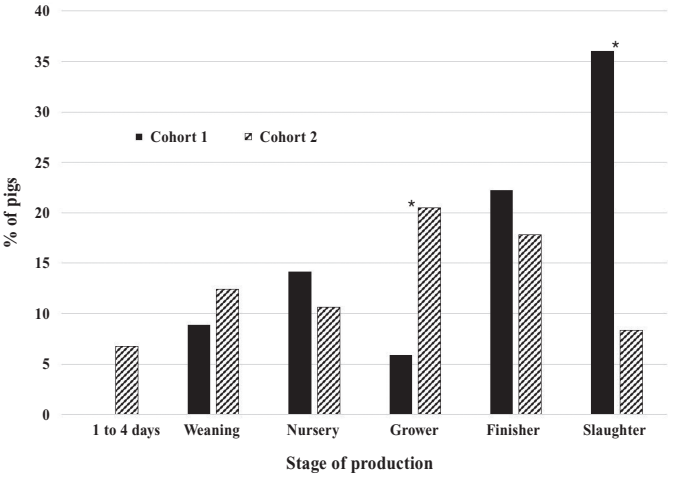

Figure 1. Proportion of pigs testing positive for *Salmonella* in feces on farm and in tissues at slaughter in Cohort 1 and Cohort 2. Samples at 1 to 4 d of age were only collected from piglets in Cohort 1 on 2 farms (n = 112) and in Cohort 2 on 5 farms (n = 297). * — The level of *Salmonella* was significantly different between Cohort 1 and Cohort 2 at this point of sampling ($P < 0.05$).

Results

Salmonella shedding

Overall, *Salmonella* was cultured from 12.6% (421) of 3339 fecal samples collected over the course of the study. In total, 421 *Salmonella* isolates were recovered from fecal samples. Of 809 pigs, 35.1% (248) shed *Salmonella* at least once and 12.2% (99) shed on more than one occasion (Table I). These 5 pigs originated from only 2 of the 8 farrowing sources. *Salmonella* was recovered from 4.9% (20/409) of pigs at 1 to 4 d of age, 10.5% (82/784) at weaning, 12.6% (94/747) at the end of the nursery period, 12.3% (90/730) at the end of grower period, and 20.2% (135/669) at the end of finisher stage. The proportions of pigs that tested positive at each stage of production and at slaughter are shown in Figure 1.

Of 809 pigs, 77.1% (624) were tested at 4 consecutive visits between weaning and the finisher stage, identifying 15 unique shedding patterns with 7 pigs testing positive at every sampling point (Table II). Among the 624 pigs, 61.1% (381) were negative on all 4 visits and 25.4% (158) shed *Salmonella* only once either at weaning (6.3%), at the end of the nursery stage (4.8%), at the end of the grower stage (5.8%), or at the finisher stage (8.5%). All pigs that were positive for the first 3 visits were also positive at the finisher stage (1.1%) and although only 2 of these pigs were sampled at slaughter, they were both positive at slaughter.

Table II. Repeat *Salmonella* shedding patterns and presence of *Salmonella* in tissue samples at slaughter in pigs sampled from weaning to finisher period (*n* = 624).

Number (%) of pigs	*Salmonella* fecal shedding				*Salmonella* in tissues at slaughter; number (%) of pigs	
	Weaning	Nursery	Grower	Finisher	Positive	Total
7 (1.1)	■	■	■	■	2 (100)	2
4 (0.6)	■	■	□	■	1 (50.0)	2
4 (0.6)	■	■	□	□	1 (33.3)	3
3 (0.5)	■	□	■	■	1 (33.3)	3
4 (0.6)	■	□	■	□	0 (0)	4
13 (2.1)	■	□	□	■	5 (50.0)	10
39 (6.3)	■	□	□	□	3 (9.4)	32
8 (1.3)	□	■	■	■	3 (60.0)	5
4 (0.6)	□	■	■	□	1 (25.0)	4
21 (3.4)	□	■	□	■	5 (41.6)	12
30 (4.8)	□	■	□	□	10 (34.5)	29
17 (2.7)	□	□	■	■	5 (33.3)	15
36 (5.8)	□	□	■	□	7 (20.0)	35
53 (8.5)	□	□	□	■	23 (53.5)	43
381 (61.1)	□	□	□	□	47 (14.5)	324
624 (100)						

■ Positive □ Negative

Of the 686 pigs that were followed through to slaughter, 580 were sampled at slaughter. Sixty-one pigs could not be sampled due to early processing and 45 pigs were missed on the line due to lost ear tags. Overall, *Salmonella* was cultured from 19.2% (109/567) of tonsil samples and 20.7% (92/445) of lymph node samples collected at slaughter; 23.1% (134/580) of pigs tested positive in at least one tissue sample. In total, 201 *Salmonella* isolates were recovered from tissue samples at slaughter. Of the 580 pigs sampled at slaughter, 563 had a sample collected at the finisher visit, approximately 2 wk prior. Out of the 100 pigs that shed *Salmonella* in feces at the finisher visit, 50% (50) of pigs tested positive in tissues at slaughter. Out of 463 pigs negative for *Salmonella* shedding at the finisher visit, 17.5% (81) tested positive in tissues at slaughter.

Multivariable analysis

***Salmonella* shedding on farm.** Independent variables selected in the univariable analysis for initial inclusion in the final model were nursery diet, season, age, gender, and number of pigs in the finisher barn (herd size). The multivariable analysis is shown in Table III. *Salmonella* shedding did not differ between pigs that received the low or high complexity nursery diets ($P > 0.05$). However, *Salmonella* shedding increased over time with older pigs more likely to test positive ($P = 0.014$). In addition, samples collected in the winter were less likely to test positive than those collected in the fall ($P < 0.001$) and samples collected in the summer were more likely to test positive than ones collected in the fall ($P < 0.001$). Furthermore, pigs from Cohort 2 were more likely to shed *Salmonella* than pigs from Cohort 1 (OR = 4.26, $P = 0.012$). There was no confounding variable identified but there was an interaction between season and age. Variation in *Salmonella* shedding due to farm and pig effects (repeated measurement) was 53% and 47% of the total variation in the model, respectively; variation due to the sow effect, however, was less than 0.1%.

***Salmonella* at slaughter.** Independent variables selected in the univariable analysis for initial inclusion in the final model were age, zinc use, cohort, nursery diet, and season. In the final model, age and cohort were significantly associated with the presence of *Salmonella* in either palatine tonsils or submandibular lymph nodes collected at slaughter (Table IV). Older pigs were less likely to test positive for *Salmonella* at slaughter ($P = 0.017$), as were pigs from Cohort 2 (OR = 0.16, $P < 0.001$). There was no association between shedding *Salmonella* on farm and the isolation of *Salmonella* from tissue at slaughter. There was no confounding variable and no significant interactions were identified. The variation in *Salmonella* isolation from tissue samples collected at slaughter due to farm and sow

Table III. Mixed-effects multivariable logistic regression analysis of *Salmonella* shedding across the production stages for 14 groups of pigs (N = 809) originating from 8 distinct farrowing sources.

	OR	SE	95% CI	*P*-value
Cohort				
1	Referent			
2	4.26	2.47	1.37, 13.27	0.012
Season				
Fall	Referent			
Spring	0.53	0.55	0.07, 4.04	0.542
Summer	19.2	14.09	4.55, 80.94	< 0.001
Winter	0.01	0.01	0.00, 0.06	< 0.001
Age (wk)	1.10	0.04	1.02, 1.19	0.014
Season * age				
Spring * age	0.94	0.07	0.80, 1.10	0.434
Summer * age	0.74	0.04	0.66, 0.83	< 0.001
Winter * age	1.22	0.08	1.08, 1.38	0.002

CI — confidence interval; OR — odds ratio; SE — standard error.

effects was 77% and 23% of the total variation in the model, respectively. In the 2 separate models fitted with "presence of *Salmonella* in tonsils" and "presence of *Salmonella* in submandibular lymph nodes" as dependent variables, the number of times a pig shed *Salmonella* on the farm was borderline significant with the presence of *Salmonella* in tonsils (OR = 1.41, $P = 0.062$). However, fecal shedding showed no significant influence on the presence of *Salmonella* in submandibular lymph nodes.

Discussion

This study set out to characterize *Salmonella* shedding from birth to market, as well as compare on farm shedding with the presence of *Salmonella* in tissue samples collected at slaughter.

Overall, there was an increase in *Salmonella* shedding from early life to the finisher stage. This is in contrast with studies that report shedding to peak during the nursery period and subsequently decrease over time (16,17). However, similar to the present study, Dorr et al (18) found that the proportion of pigs shedding *Salmonella* increased from the end of the nursery period until slaughter. One explanation is that as time progressed, unexposed pigs may have become exposed to *Salmonella*, while previously infected pigs may have been infected by a new serotype (16). In fact, a recent feed additive clinical trial study performed on commercial pigs from southwestern Ontario found that pigs with repeated infections had as many as 8 different serotypes over the studied period (19). In the current study, 12 of the 14 groups of pigs were shipped to an off-site weaning barn and 13 of the 14 groups were shipped to an off-site grower-finisher barn. Shipping and comingling of pigs is known to cause stress and thus, provide an opportunity for the spread of disease (20). Nollet et al (21) found the number of pigs shedding *Salmonella* increased significantly after transportation to a second facility and transportation stress has been shown to cause recrudescent shedding in pigs experimentally infected with *Salmonella* DT104

Table IV. Mixed-effects multivariable logistic regression analysis of the presence of *Salmonella* in tissues for 13 groups of pigs (*n* = 580) originating from 7 distinct farrowing sources.

	OR	SE	95% CI	*P*-value
Cohort				
1	Referent			
2	0.16	0.05	0.08, 0.31	< 0.001
Age (wk)	0.77	0.08	0.62, 0.95	0.017

CI — confidence interval; OR — odds ratio; SE — standard error.

(22). In the current study, 12% of pigs shed *Salmonella* repeatedly. Regardless of whether these pigs shed one serotype chronically or multiple serotypes, they all represent an important source of contamination to the environment and other pigs. In fact, semi-stochastic models demonstrate that a single infected pig can spread *Salmonella* that persists within the barn environment (23). The comingling and movements of the numerous pigs observed in this study are reflective of commercial farming in Ontario, as the number of swine farms owned by corporations are increasing and farms or contract producers are becoming more specialized (24).

The impact of season on *Salmonella* shedding observed in the present study was not unexpected, as summer has previously been reported to be a risk factor for the presence of *Salmonella* in pig herds (25). In addition, the interaction between season and age could be explained by the fact that pigs were born in clusters between May and August or October and January and then followed for 6 mo.

Salmonella shedding in pigs differed between the 2 cohorts, which highlights how important it is to monitor farms for the presence of *Salmonella* over time. The "cohort" variable was included in the analysis to account for unmeasurable differences between cohorts from the same farrowing source. There was approximately a 6-month gap between the first visit for Cohorts 1 and 2 on each farm, meaning that many pigs from unknown sources and with unknown health challenges passed through the barns. Although the farrowing sources and nursery sites were identical for each farm between the 2 cohorts, the operations used different locations for the grower-finisher barns and thus, pigs in different cohorts experienced different shipping times and conditions, which may also explain variation in the presence of *Salmonella* at slaughter between the 2 cohorts. Pigs from the first cohort on one farm never tested positive for *Salmonella*, while shedding in the second cohort of pigs from that farm peaked in the nursery period and subsequently declined until slaughter. It should be noted that this farm was the only antibiotic-free farm, which might influence *Salmonella* transmission in pigs on this farm.

Presence of *Salmonella* in tissues at slaughter was not significantly associated with on farm fecal shedding; the number of times an animal shed and shedding at each stage analyzed independently had no influence on the presence of *Salmonella* in tissue samples collected at slaughter. This finding adds to the growing body of literature reporting a poor association between fecal culture of *Salmonella* on farm and its isolation from internal tissue samples at slaughter (11,12,16,26). Although it has been shown that pigs infected later in life had an increased risk of carcass contamination at slaughter compared with pigs infected earlier in life (10), in this study, the

presence of *Salmonella* in tissue samples collected at slaughter was not associated with fecal shedding at the finisher stage.

It is reasonable for pigs that tested positive in the finisher period to remain positive at slaughter. *Salmonella* can colonize the tonsillar crypt cells and invade systemically, appearing hours later in the gut, internal organs, and lymph nodes (27). The fact that the fecal-oral route is the most common route of infection in swine (20) may explain why *Salmonella* could be recovered from the tonsils of pigs that shed *Salmonella* on farm. Additionally, pigs which shed *Salmonella* on farm may have *Salmonella* in their lymph nodes at slaughter, since the detection and transference of bacteria to the lymph nodes by antigen-presenting cells is part of a normal immune response to the pathogen (28). Finally, these pigs could have come into contact with an additional serotype during transportation and lairage (12).

Furthermore, pigs that tested negative in the finisher period could have been tissue negative at slaughter because they might have cleared an infection, leading to a robust immunity to the pathogen, or they simply might not have been exposed to *Salmonella* before processing and sample collection. As for animals that were positive at the finisher period but negative at slaughter, it is possible that they were infected with a serotype that is only capable of colonizing the gut, but not capable of colonizing the tonsil or causing systemic infection (29,30). For pigs that were negative on farm but positive at slaughter, 2 possibilities exist. It is possible that the pigs were free of infection on the farm and picked up the bacteria during transportation to slaughter or while being held overnight (12,31). Alternatively, these pigs might have been colonized with *Salmonella* on farm and shed intermittently or at undetectable levels but the stress of transportation increased shedding (22,32,33). It is possible that the pigs did not shed bacteria at the time of sampling or that they were misclassified as negative due to undetectable levels of *Salmonella* given the sampling and culture techniques used, although, the use of 3 selective media in this study greatly improved the sensitivity of culture techniques (34,35).

To the best of our knowledge, this is the first study to repeatedly sample such a large group of pigs from birth until slaughter. Although it is possible that pigs were positive at other times not sampled, sampling each pig at 5 time points and at slaughter provides new information on the epidemiology of *Salmonella* infection in swine.

In the current study, *Salmonella* shedding increased as pigs became older. Although previous research has shown the nursery period to be the peak of shedding, it may be prudent from a food safety perspective to evaluate risk factors and interventions that help mitigate *Salmonella* shedding at later stages of production. However, the presence of repeat shedders and the lack of association between *Salmonella* shedding on farm and its presence in tissues at slaughter is a food safety concern that warrants attention to implement control measures at the slaughter level. Future studies should investigate the serotype and molecular characteristics of *Salmonella* isolates to better understand the dynamics of *Salmonella* shedding on swine farms.

Acknowledgments

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